

REMARKS

Status of the Claims

Pending claims

Claims 1-33 as filed are pending.

Claim amendments in the instant response

Claims 1 and 2 are amended. Claim 34 is added.

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JUN 13 2002

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Support for the Claim Amendments

The specification sets forth an extensive description of the invention in the new and amended claims. Support for the new claim directed to identifying nucleic acid sequences or polypeptide sequences with the desired property by identifying functional relationships to a first sequence known to possess the property can be found, *inter alia*, on page 2, lines 7-8; page 7, lines 21-28; and claims 1 and 2, as originally filed. The amendments to claims 1 and 2 merely make them dependent claims of the generic new claim 34. No new matter has been introduced by the instant amendments.

The Restriction Requirement

The Patent Office has alleged that the pending claims of the application are directed to five separate and distinct inventions under 35 U.S.C. §121, as follows:

I. Claims 1, 3-30, drawn to a method for identifying a nucleic acid or a polypeptide sequence that may be a target for a drug, classified in class 435, subclass 6.

II. Claims 2-30, drawn to a method for identifying a nucleic acid or a polypeptide sequence that may be essential for the growth or variability of an organism, classified in class 435, subclass 7.1.

III. Claim 31, drawn to a computer program for identifying a nucleic acid or a polypeptide sequence that may be a target for a drug, classified in class 707, subclass 1.

IV. Claim 32, drawn to a computer program for identifying a nucleic acid or a polypeptide sequence that may be essential for the growth or variability of an organism, classified in class 707, subclass 1.

V. Claim 33, drawn to a computer system, classified in class 711, subclass 1.

The Election with Traverse

In response to the Restriction Requirement, Applicants elect with traverse the invention of Group I drawn to a method for identifying a nucleic acid or a polypeptide sequence that may be a target for a drug, classified in class 436, subclass 6.

Applicants have introduced new claim 34, which provides a generic claim for the species claims in Groups I and II. Applicants respectfully request that Groups I and II be examined together.

Responsive to the office action mailed May 10, 2002, the Restriction Requirement with respect to the claims is traversed on several grounds. In particular, with respect to the methods of Groups I and II, as set forth in new generic claim 34, the methods of the invention utilize the steps of providing a first known nucleic acid or polypeptide sequence; providing at least one algorithm selected from the group consisting of "domain fusion," "phylogenetic profile," and "physiologic linkage;" and comparing the first known sequence to a plurality of sequences using at least one of the algorithms to identify a second sequence that has a functional relationship to the first sequence. Therefore, while the property of interest of the first sequences may differ (as selected by the user, *e.g.*, to identify a drug target or a gene essential for growth), the steps to arrive at the functional relationship between the first and a second sequence remain the same. This relationship between the claims is clarified by generic claim 34 (claims 1 and 2 both depend from claim 34). Accordingly, the subject matter of originally filed claims 1 and 2 overlap and,

especially in light of new genus claim 34, a search and examination of the methods of Groups I and II together would not constitute an undue burden on the Examiner.

Moreover, Applicants submit that the invention set forth in claims 31 and 32 of Groups III and IV comprise the methods of Groups I and II, respectively, in the form of a computer program. A search of the methods of Groups I and II should yield art in the field of computer programs that utilize such methods, as computer programs comprise a compilation of steps of a method in a computer readable format. Accordingly, the subject matter of the claims overlap and a search/examination of the methods and the methods as part of a computer program would not constitute an undue burden on the Examiner.

Applicants further submit that the invention as set forth in claim 33 of Group V comprises the computer program of claims 31 and 32 in a computer system. Accordingly, the subject matter of the claims overlap and the examination/search of the method claims as a computer program or in a computer system should not constitute an undue burden on the Examiner.

Thus, for the reasons set forth above, Applicants respectfully request that the Patent Office reconsider the restriction requirement and rejoin Groups I, II, III, IV, and V to be examined together.

Applicants believe that no fee is required for submission of this Response. However, if a fee is required, the Commissioner is authorized to deduct such fee from the undersigned's Deposit Account No. 06-1050. Please credit any overpayment to the above-noted Deposit Account.

Applicant : Eisenberg et al.
Serial No. : 09/712,363
Filed : November 13, 2000
Page : 6

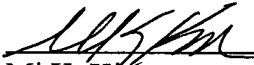
Attorney's Docket No.: 07419-032001 / LA99-566-6

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 858 678 5070.

Attached is the Version with Markings to Show Changes Made.

Respectfully submitted,

Date: June 6, 2002


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Version with Markings to Show Changes Made

In The Claims:

Please replace claims 1 and 2 with the following rewritten claims:

1. (Amended) The method of claim 34, wherein the property of interest of the first sequence is [A method for identifying a nucleic acid or a polypeptide sequence that may be] a target for a drug [comprising the following steps:

(a) providing a first nucleic acid or a polypeptide sequence that is known to be a drug target;

(b) providing at least one algorithm selected from the group consisting of a “domain fusion” method, a “phylogenetic profile” method and a “physiologic linkage” method, wherein the algorithm is capable of analyzing a functional relationship between nucleic acid or polypeptide sequences; and

(c) comparing the first nucleic acid or the polypeptide drug target sequence to a plurality of sequences using at least one of the algorithms as set forth in step (b) to identify a second sequence that has a functional relationship to the first sequence, thereby identifying a nucleic acid or polypeptide sequence that may be a target for a drug].

2. (Amended) The method of claim 34, wherein the property of interest of the first sequence is a sequence [A method for identifying a nucleic acid or a polypeptide sequence that may be] essential for the growth or viability of an organism [comprising the following steps:

(a) providing a first nucleic acid or a polypeptide sequence that is known to be essential for the growth or viability of an organism;

(b) providing at least one algorithm capable analyzing a functional relationship between nucleic acid or polypeptide sequences selected from the group consisting of a “domain fusion” method, a “phylogenetic profile” method and a “physiologic linkage” method; and

(c) comparing the first nucleic acid or the polypeptide sequence to a plurality of sequences using at least one of the algorithms as set forth in step (b) to identify a second sequence that has a functional relationship to the first sequence, thereby identifying a nucleic acid or polypeptide sequence that may be essential for the growth or viability of an organism].